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Db 121 GGRGAFGRGAEYVISPJPNASAPAAQNSOGAHLQRRVGPSPTRSGVASCW 180
Oy 181 NPATLALDPYPRRAGSESRSSRRSGAKRFPVSPRVELLVVADESMVFRGADLEH 240
Db 181 NPATLALDPYPRRAGSESRSSRRSGAKRFPVSPRVELLVVADESMVFRGADLEH 240
Oy 241 YLLTLATLAAALYRHRPSILNPINIVVVKVLLLRDRDSGPKVGNALTRNCAMOKLN 300
Db 241 YLLTLATLAAALYRHRPSILNPINIVVVKVLLLRDRDSGPKVGNALTRNCAMOKLN 300
Oy 301 KVSADKHEVMDALFTFRODLGATTCDTLGMADVTCMDPRSCSVIEDDLPSAFTTA 360
Db 301 KVSADKHEVMDALFTFRODLGATTCDTLGMADVTCMDPRSCSVIEDDLPSAFTTA 360
Oy 361 HELGHVFNPHNVKCEVFGKLRANHMSPITLQIDRANWMSASAIIITDFLDSHG 420
Db 361 HELGHVFNPHNVKCEVFGKLRANHMSPITLQIDRANWMSASAIIITDFLDSHG 420
Oy 421 DCLLDOPSKPISLPEDLPASVYTLSSQCELAFAVGSKPCPYMQYCTKLMCTGAKAGMVC 480
Db 421 DCLLDOPSKPISLPEDLPASVYTLSSQCELAFAVGSKPCPYMQYCTKLMCTGAKAGMVC 480
Oy 481 QTRHFPADGTSQSGKGLCKAGCYERHNLKRVDSMAKMDPYGCSRTCGGCVQLAR 540
Db 481 QTRHFPADGTSQSGKGLCKAGCYERHNLKRVDSMAKMDPYGCSRTCGGCVQLAR 540
Oy 541 RQCTNPPTANGKGYEGVAVKYSNLEPSPSSAGSKFREPQCAFNGYNHSTRLTLA 600
Db 541 RQCTNPPTANGKGYEGVAVKYSNLEPSPSSAGSKFREPQCAFNGYNHSTRLTLA 600
Oy 601 VAWVKYSGVSPRDKCKLICRANGTYGYVLA PKVVDGTLSPDSTSVYQVQKCIKACD 660
Db 601 VAWVKYSGVSPRDKCKLICRANGTYGYVLA PKVVDGTLSPDSTSVYQVQKCIKACD 660
Oy 661 GNLGSKRRFDKCGVCGGNKSKKVTGLFTKPMHGYNFVAIPGASSIDIRORXYKLI 720
Db 661 GNLGSKRRFDKCGVCGGNKSKKVTGLFTKPMHGYNFVAIPGASSIDIRORXYKLI 720
Oy 721 GDNNTLALNKSOGKYLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILTELT 780
Db 721 GDNNTLALNKSOGKYLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILTELT 780
Oy 781 VEIVSVGKMPPRVRYSTYLPKEPEDKSSHPKDPGRGSVLAHNSVLSLNQVEQPDPRP 840
Db 781 VEIVSVGKMPPRVRYSTYLPKEPEDKSSHPKDPGRGSVLAHNSVLSLNQVEQPDPRP 840
Oy 841 ARWVAGSWGSPASGSGSLQKRAVDCRGSAGORTVPACDAHARPVETQAGEPCPTWELS 900
Db 841 ARWVAGSWGSPASGSGSLQKRAVDCRGSAGORTVPACDAHARPVETQAGEPCPTWELS 900
Oy 901 AWSPCSCKGGRFORSILKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 950
Db 901 AWSPCSCKGGRFORSILKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 950

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RESULT 2

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Oy 091256 PRELIMINARY; PRT; 340 AA.
AC 091256;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Similar to a disintegrin and metalloproteinase with thrombospondin
motifs 1 (Adams-1) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL: BC009667; AA09667.1;
DR InterPro: IPR000884; TSP1.
DR Pfam: PF00090; tsp_1; 2.
KW Integrin.
FT NON_TER 1 1
SQ SEQUENCE 340 AA; 37021 MW; 06562C747634A8BD CRC64;

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Query Match 32.6%; Score 1685; DB 11; Length 340;
Best Local Similarity 91.7%; Pred. NO. 9.5e-132;
Matches 308; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

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Oy 615 KCKLICRANGTYGYVLA PKVVDGTLSPDSTSVYQVQKCIKACDGNLGSKKRFPDGV 674
Db 5 KCKLICRANGTYGYVLA PKVVDGTLCPDSTSVYQVQKCIKACDGNLGSKKRFPDGV 64
Oy 675 CGDNKSKKVTGLFTKPMHGYNFVAIPAGASSIDIRORGYKGLIGDNTLALNKSQK 734
Db 65 CGDNKSKKVTGLFTKPMHGYNFVAIPAGASSIDIRORGYKGLIGDNTLALNKSQK 124
Oy 735 YLLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILTELTVEIVSVGKMPPRV 794
Db 125 YLLNGHFVSAVERDLVYKSLRYSGTGAVESLQASRPILTELTVEIVSVGKMPPRV 184
Oy 795 RYSEYLPKEPEDKSSHPKDPGRGSVLAHNSVLSLNQVEQPDPRPARWVAGSWGSPAS 854
Db 185 RYSEYLPKEPEDKSTRPKDPRGSLVLAHNSVLSLNQVEQPDPRPARWVAGSWGSPAS 244
Oy 855 CGSLQKRAVDCRGSAGORTVPACDAHARPVETQAGEPCPTWELAWSPCSCKGRGQ 914
Db 245 CGSLQKRAVDCRGSAGORTVPACDAHARPVETQAGEPCPTWELAWSPCSCKGRGQ 304
Oy 915 RRSILKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 950
Db 305 RRSILKCYHGGRILIARDQCNLHRRPQELDFCVLRPC 340

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RESULT 3

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Oy 019791 PRELIMINARY; PRT; 2165 AA.
AC 019791; 027524;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F25H8.3 protein.
DE F25H8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gajadasy S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Shaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Welstock L., Wilkinson-Spoat J., Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans."
RL Nature 368:32-38(1994).
DR EMBL: Z69361; CAA93288.1;
DR EMBL: Z69360; CAA93288.1; JOINED.
DR EMBL: Z69360; CAA93287.1;
DR EMBL: Z69361; CAA93287.1; JOINED.

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QY	481	QTRHFPADGTSICGGGKCLTCLGACVERHNLNKKHVDGSMAMKDPYGPCSRTCGGGVQLAR	540
Db	553	ERKFMPEAGIEVYCGISLMACRGQOCYKFEGLDPRPIHGWSMWSKWSCTRTCGGGVAFQE	612
QY	541	ROCTWPTPANGKCYKEGVRYVYRSGNLEPCPSSASGKSFREOCEAEN-----GYNSTN	595
Db	613	RHCNNPKQYGGIFPCPGSSRTYQULCNINPC--NENSIDFRQOQCAETNSKPFKMFYQ--	668
QY	556	RLTLAVAWPKYSGVSPDKCKLICRANGCYFYVLAPKVVDTGLCPDSTSYCVQGGCI	655
Db	669	-----WKP--YTKVEEDRCKLYCKAENFEFFPAMSGKYVDGTPCSPNKNDYCIDQVCE	720
QY	656	KAGCGDNGSKKRPDKCGVCGGDMKSOCKKTYGLTK--PMHGIFYVAIPAGASSDIDQ	713
Db	721	LVGCHHEIGSKRAVSDACVCGDGNSTCKFKKGLYNLHKANEYYPVLLIPAGARSIEIOE	780
QY	714	RGYKGLIDDDMYLALKNQGYKLLNGHFVSAVERDIYVGSILRYSGTGAVESILOASR	773
Db	781	-----LQVSSSYLAVRSLQKTYLILGMSID-WGGEPPFAGTTFEYGRSNRRERLXAPG	834
QY	774	PILEPLIVYEVLSVGKMPPRVRYISFYLPK-----EPREDK-----SSHKDPKPGSV	820
Db	835	PTNEFLVLEILLMOGR--NPGIAMRYALPKWANGTPATKRPATYATWSIVQSECVSGGGY	892
QY	821	LHNSVLSISNVOEQ-----LPDRP-----PARWAGSGPCSASCGSGLOK	861
Db	893	INVAICALRDNTQVNSFCSAKTKPTPERICINAFESCPAYMFMGEMSTSKSCAGGQS	952
QY	862	RAVDCRGASGAGRTYPA-----CDAHRPVTQAC-GEPC-PTWELSAMSPCSKSCGRGQ	914
Db	953	RKIOCVOKRPQKEAEVYLHSICLPPS-TPTOYACNSHACPPQWSILGFWSCSKTCGRGV	1011
QY	915	RSLSKCVGHGGRLIARDQCNHRRPOELDQVLCAPC	950
Db	1012	KRELLCKGSAEATLPESQCTSLPRPELQGVLCGR	1047
RESULT 5			
ID	Q8TE57	PRELIMINARY;	PRT; 1072 AA.
AC	Q8TE57;		
DT	01-JUN-2002 (TREMBlrel, 21, Created)		
DT	01-JUN-2002 (TREMBlrel, 21, Last sequence update)		
DT	01-JUN-2002 (TREMBlrel, 21, Last annotation update)		
DE	Metalloprotease disintegrin 16 with thrombospondin type I motif.		
GN	ADAMTS16.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	11		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-21856482; PubMed-11867212;		
RA	Cal S., Odaya A.J., Llamazares M., Garabaya C., Quesada V.,		
RA	Lopez-Otin C.;		
RT	"Cloning, expression analysis, and structural characterization of		
RT	seven novel human ADAMTS, a family of metalloproteinases with		
RT	disintegrin and thrombospondin-1 domains."		
RL	Gene 283:49-62(2002)		
RM	EMBL, AJ315734; CAC86015.1; -.		
TM	Integlin; Protease.		
SQ	SEQUENCE 1072 AA; 081EEFF78F47D061 CRC64;		

	Query Match	24.2%	Score 1247.5;	DB 4;	Length 1072;
	Best Local Similarity	32.9%	Pred. No. 1.3e-94;		
	Matches	332;	Conservative 126;	Mismatches 386;	Indels 165; Gaps 38;
OY	51	QGLIQTITAFDEDFYLHLPDAQFLAPAFSTENHLGVPLOGLTGGSS-----DLRRCFY	103		
	:	: : : : : :	:	:	:
	:	: : : : : :	:	:	:
Db	95	ESTLIRLRKGRPRDFMDRTSSSLVAPGFIVOTL-----GKGTGSVSOTLPPEDEF--CFY	147		
OY	104	SGDVAAEDPSFAANVLSCGLRGAEFGYRCRAEYVISPLPNASAPAAQRNSOG---AHILQRR	160		

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Db 148 QSLSHSHRNSVALSTOCGLSMINTBEADYFLRPLRPLSHLSWKLGRAOGSSPSHVLYKR 207
Qy 161 G-----VPGGSPGSDPISR-----CGVASGNMFA-----TLRA 187
Db 208 STEPHAPGASEVLYMSTRWELAHQOLHSSDRLRLGPKQHRCGRKKYMPQRPKEDEFL 267
Qy 188 LDPYKPRRARGPEBSRRRRSGRAKFFVSIPIKVELIYVADESMVKFNG-ADLEHYLTLL 246
Db 268 PEYK---SCLRHKSSLRLSHRNEEL-----NVELIYVADKKMONGHENHETIYVLTIL 319
Qy 247 ATAARLYRPSILININIVYVAVLLRLRDRDGPCKTGAALTLTKNFAWOKKL-NKYSK 305
Db 320 MNVSAFLPDGTIGGININAIYGLILBEDOGLVISHADITLSPFOMOSGLMGKRGTR 379
Qy 306 HPEYDOTALITRDLG--ATTCDTLGMADVYTWCDPKRCSYIEDGLPSAETTAAHEL 363
Db 380 H-----DHAILTLGLDICSWMKNEPCDTLGFAPISGCSKYRSCITNEDTGLAFTIAHES 435
Qy 364 GIVEFMMPHDNV-KVCEEVFGKIRANHHMSPILIODIRANPMSACSAIITDFLDSGDC 422
Db 436 GNFMGAIHIDBGMCKKSEG-----NIMSPLAGNVSFSPSCROYLHKFLSTAOAIC 490
Qy 423 LIDQSKPI--SLPEDLPGASVYTLSDQCELAFGVSGPCPY--MOYTKLMC--TGKA 474
Db 491 IADQ--KPYEKYKYPEKJGELYDANTQCKMQPEBKAKLCLMDLCKDICAKMOHRIGRK 549
Qy 475 KQAMVCOTRHPMADGTCSGEGSKLCKGACYERINLNKHRDGSWAKWDPYGCSPRCGG 534
Db 550 -----CEIKFMPAAEGTICGHDMMCRGGQCVKYADEGCRPTHGHSWSSMSWSPCSRGG 604
Qy 535 GYOLARROCTPPTPANGGKCYEVYVYRSCNLEPCPSASAGKFFREOC-----EAFNG 589
Db 605 GYSHSRICSTNPKPSHGKPCBGSTRIKLKCNOSKCRDS--VDFRAQCAEINSRFRG 662
Qy 590 YNHSTNRLTLVAVMPKYSVSPDKCKLICRANGTGYFYVADKVVDTGLCSPDSTVC 649
Db 663 RHYK-----WKP-YTQVEDDOLCKLYCIAEGFFEFSLSKMYKDKGTPCSEDSHNV 712
Qy 650 VQKCIKAGCGGNIGSKRPRKPCVCGGDNSCKKVTGLTFKPNH--GYMFWAIPAAGS 707
Db 713 IDGICERGVCDNVLASDAVEYCVGCMGNNSACTIHRGLYTKHNHTNOYHMTIISGAR 772
Qy 708 SLIDIKORYKGLIGDNNLTALKNOSQVYLNHGFVSAVERDLVYKSSLYRGSGTAVE 767
Db 773 SIRIEMNV-----STISIVRNALRLRYLNGHMTVMPGR-YKFSOTTFDYRSTNEPE 826
Qy 768 SLQASRPLLEPLIYEVLSVGKMPPRVRSFYFLRKEPREDKSSHKDPKPS-----819
Db 827 NLIATGPNTELIVELLEPOGR--NPGVAMEWSMP-----LGTGKOPAPQSTYMAIVAS* 879
Qy 820 -----VLHNSTLISLNOVE-----QPRDR-----PARWAGSGMGC 851
Db 880 ECSVSCGGGQMTYVDEGCYRDLKFOYNNMSPCNKTRPTGTGLPCKVSAACPSSWVGWMSAC 939
Qy 852 SASCGSGLOKRAVDC--RGSAGORTVA--CDAAHRPVETQAC-GEBC-PTWELSAMSP 905
Db 940 SRTCGGAGSPVQCTRVHVDSPVASYLCQDQ-APSSQACNCSGCPRAWASGPMWAE 998
Qy 906 SKSGRGQRORSKLACVGHG-----GRLLARDOCNLHRRPOELDPCVLRPC 950
Db 999 SHTQCGKRRKRAVACKSTNPSARQOLLPDAVCTSEPPRHNKACLQRC 1047

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RESULT	6
Q8SXBO	
ID	Q8SXBO
AC	Q8SXBO;
DT	01-JUN-2002 (TREMblrel. 21, Created)
DT	01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT	01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE	GH6393p.
NN	CG6107.


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Db 348 CVHKDEPDVGVIAVLGGVCSAKRRCVLAENGLMAFTIAHEIHLNLMNH-----DD 402
OY 380 VEGKLRANHHMSPPTLIQIDRANP-----WSACSAIITDFELSGHDCLL-----DPSKIPS 432
Db 403 HSSCGRSHINGEMVW--GRNPDLMSSSCSRDLENFLSKYSTCLLVDPRQHTVR 460
OY 433 LPEDIPGASVTLSDQCELAFGVSKPCPYMOT--CTKIMCTGKAKGAWVCOTRHPPMADG 490
Db 461 LPHKIPGHHYSANEGCQILFGKNMATEFCRMHELMCAGLMCL--VGDPTSCRTKLDPPLDG 518
OY 491 TSCGEGKCLTGACVYERNNLNKHNKRDGSMARKDPRGCSRTCCGGVQOLARQCTPTPAN 550
Db 519 TEGCGADKRCRAGECVSKPIPEH--VDGWSFPGAWMSRFGCTGARPRORCDNPPGP 577
OY 551 GKYCEGVVYVYRSCNLEPCSSASGSKSFRBEOCEAFNGYNHSTRLTLAVAVMPKYSGV 610
Db 578 GGTGPGASVEHVAENLPCPKGL--PSFRQCCGAHRLSKKKGLLAV-----V 627
OY 611 SPRDKCLICRANGTYTYVLAIPKVVYDGLSPDSTSYCVGCKIKACDGNLSKKRPD 670
Db 628 VDDKPCELYCSPDKSEPLVADRVLDTGPGPYETDLGVHGKCKICDGLIGSAKED 687
OY 671 KGVCGGDNKSCCKVTGFTKPMHGNFVVAIPAGASSIDIRORGYKGLIGDNYLAKN 730
Db 688 RGVCSGSGKCHLVKGFPSH-----ARGTALKDSG-KGSI-----N 723
OY 731 SGGKYLNGHFVSAVERDLVVKSLRYSGTGAVESILOASRPILPELTYEVL-----S 785
Db 724 SDMKTELEGEFOIA-----GTTYRYVRRG-LMEKISAKGPKLPLHMLVLLFHDQD 773
OY 786 VGKMPRPVRYRSTYLPKPRFREDKSHPKDPR-----GTSV----- 820
Db 774 YG-----IHEYYVAVNRVIAENQSEPEKPODSLFIWTHSGWEGSGVGGGERRTIYSC 827
OY 821 --LHNSVLSLNOVEOPDPRP-----ARVAVAGSWGPCSCSGSGLQKRAVD 865
Db 828 TRIYKKTITVLVNDSCCPASRPBEPQVRCNLHPQOSRNVAPWMSCSATCEKGQHRVYT 887
OY 866 C---RGSAGRTVPACDAHRPVETOAC--GEPC-PTWELSAMSPCSKRGFGORSLK 919
Db 888 CVYQLONGTHVATRLPYCPGRPAVQSCGQDCISIWESWESQSCSGKGVWKRTVA 947
OY 920 CVHGGRLLARDQCNLHKRPDLDFC 945
Db 948 CTNSQK-----CDASTRPAERAC 967

RESULT 8
O9VF61 PRELIMINARY; PRT; 1229 AA.
ID O9VF61 AC O9VF61;
AC 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CG6107 protein.
OS CG6107.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brooksstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Padlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idegawa C.,
RA Jaitel M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mohrson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zavei J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003709; AAF55199.1; -.
DR FLYBase: FBgn0038340; CG6107.
DR InterPro: IPR002870; pep_M12B_proprep.
DR InterPro: IPR001590; Repolysin.
DR InterPro: IPR000884; TSPL.
DR InterPro: IPR000130; Zn_MTPetase.
DR Pfam: PF01562; pep_M12B_proprep; 1.
DR Pfam: PF01421; Repolysin; 1.
DR Pfam: PF00090; tsp_1; 2.
DR SMART: SM00209; TSPL; 3.
DR PROSITE: PSS00215; ADAM_MEPPO; 2.
DR PROSITE: PSS0092; TSPL; 2.
DR PROSITE: PSS00142; ZINC_PROTEASE; 1.
DR Hydrolase: Metalloprotease; Zinc.
SQ SEQUENCE 1229 AA; 138136 MW; C1293180AB19B700 CRC64;

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Query Match 23.4%; Score 1206.5; DB 5; Length 1229;
 Best Local Similarity 32.0%; Pred. No. 4.2e-91;
 Matches 321; Conservative 140; Mismatches 329; Indels 213; Gaps 43;

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OY 55 FOITAFQEDFYLIHTPPAOFIAPAFSTHGLGVPLQ-----LTGSSDLRR--CFYSGD 106
Db 195 YNLNVFQRQLHLVLRQDASV--HNHSMTHIRILKEGHEHCPRELAARDRHLCGFSGY 253
OY 107 VNAEPDSFAVSLCGIGRGAFYGAETVSPDPNASP-----AAORNSGAHLQ 158
Db 254 VEDDPHSMVSVSLCGGWTGYIKTSFGALLIOPVWRTSSDEVILHRVFKRSORNAR--HAYS 311
OY 159 RRGVPGSPGSPGPRSGVAGSWNNALRALDPYPRRAGCE-----SRSRRSRGRAKRFV 214
Db 312 KFEI-----GDDDEFSKIEQVOEEOBKSRKLNKRHHYA 347
OY 215 SIPRYV--ETLVVADESNVKEFGADLEHVLITLATAARLYRHPSTLNPINIVVVL 271
Db 348 DVDNQVYTLVLAIVNDMSMQFHEDDQPIITLIMSVISIFADASIGNIRILLVRLIS 407
OY 272 LRDRDSGPVY--TGNALTLRNFCAGWOKRLNVSDKHPEYWDPTAILFTQDLGAT-- 325
Db 408 L-----PNINDQHSSENMELKHRCGF--INGSYER-----DTAMLTREPIGSGVPGK 454
OY 326 TCDTLGNADVGTMDPKRRSSVIEDDGLPSAFTTAHGLGVFWMPHDNVAVCEVYEGKLR 365

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Db 455 ICHMLGIAELGTVCS--SSGSIYDPTGSLPFTMAHELIILMNNHDDDDCKMPYVTRON 513
Oy 386 AN---HMMSPTL-IQIDRANPMSACSAIITDPLDSDGCLLDQPSKPISLP---EDLP 438
Db 514 NKKVLIHMSVMGIIHM---HPMSMSKK---TD-----KSCSL--EHSVGAHIPTGERLIP 559
Oy 439 GASYTSLDQOELAFGVSKRCPRYMOVCTKLWC---TGKAGGOWVCORHHPMDGTSKG- 494
Db 560 GEIYSLDADQOLSFQNDGFGYCPDEDECKRLMCNRTSGNSNDQ--CASSNLPMDGTPCGS 617
Oy 495 EGKCLTCLGACVBERHNLKH-----RVDSNAKMPDYGPCSTCGGVALAROCNTPTPAN 550
Db 618 SGHMCQKGVCS---NKHGYGRQVNGCMGMPHPTPCSLTLCGGGVQESRECNQRPEN 673
Oy 551 GKGVCSEVRYKYNSCNLEPCPPSSASGKSFREOCEAFNGYNHSTNRLTLAVANPKYSGV 610
Db 674 GKGKCTSRKKYRSCNTHOCPPSMDP--REOCCYAMNGNMNTPGYNPTKVPKYE-- 729
Oy 611 SPBDKCLIGRANGTGYEVLAPRYVDGTLCSPDSTSVCGKCIKAGCGDNLGSKKRF 670
Db 730 --RDACKLFCRMDKVTYEMLKSNVDTGSCAVDSFDCVNGICRPAGCDNELSTAKLD 787
Oy 671 KCGVCGDNKSCCKVYG-LETKPMHGYN-----FYVAIPAGASSIDIRRGYKGL 719
Db 788 KCGVCSEGRNDTCHEVTGNLNLVSNLGLDNGENPKTLTYVTRIPKASNIITITQGYV-- 845
Oy 720 IGDNNYIALKNSQGYTYLNGHFVYSAVERDLVYKGLRISGCTAVESLQA--SRPIL 777
Db 846 --DQNFYVLTDSDNELLNKF-LKTYPLKFAVAGVMQYTGSSVVEQVNTYVSMLSR 902
Oy 778 PLTYEVLVSKMTPPR-----VRSFYLPKPRR----- 806
Db 903 DLIVQITSLDVSPEKRDYVLTSTYITDKPRDYEALEYIRWEMQAPSNDCISEGRSH 962
Oy 807 -----DKSSHPR-DPRGSPV--LHNSVLSLNOVEQDDPRPARW 843
Db 963 RLPACISTTQGVKAPQFCQKSAHPKIDDRACNTDCRLNLTVISISE----- 1009
Oy 844 VAGSWGSCASGCS-GLOKRAVDC--RGSAGORP-----VPACDAHNPVETQACGECPT 896
Db 1010 -----CSAAGCGLGTREKTYACVQTFNMQRNINIDMSTCKLFDVYAHIECREG-- 1060
Oy 897 WELSAWSPSCSGRGFORSLKCVGHGRLARDOCNLHNRK 939
Db 1061 WVLSEWSTGSKSGCTGSGQREAHGTYLHNSR-VSDDLCPNRPKR 1102

RESULT 9
OyW493
ID O9W493 PRELIMINARY; PRT; 1054 AA.
AC O9W493;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CG4096 protein.
GN CG4096.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
OC Ephydroidea: Drosophilidae: Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=2016006; PubMed=10731137;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abt1 J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Broctien P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Ventler E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR HMBL; AEO03435; AAF46065.1; -.
DR HSSP; P15167; 1ATL.
DR MEROPS; M12.231; -.
DR FlyBase; FBgn0029791; CG4096.
DR Interpro; IPR002870; pep_M12B_propep.
DR Interpro; IPR001590; Reprolysin.
DR Interpro; IPR000884; TSP1.
DR Interpro; IPR001030; zn_MTPeptide.
DR Pfam; PF01562; pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP-1; 2.
DR SMART; SM00209; TSP1; 2.
DR PROSITE; PSS00215; ADAM_MERO; 1.
DR PROSITE; PSS00092; TSP1; 1.
DR PROSITE; PSS00142; ZINC_PROTEASE; UNKNOWN.1.
SQ SEQUENCE 1054 AA; 118616 MW; DC1545555C86212 CRC64;

Query Match 23.0%; Score 1186.5; DB 5; Length 1054;
Best Local Similarity 30.5%; Pred. No. 1,5e-89;
Matches 336; Conservative 140; Mismatches 375; Indels 249; Gaps 45;

Oy 17 GGFEP-----EREVVPPIRLDP-----INGRYVYR-----GPD 47
Db 23 GGVRYPLGLMSDELVAEGGLVYVRRVNPDAQFMTQOLEYAHNEIDHRRNRBSLSEHD 82
Oy 48 SGDOGILFQITAFQDEYVLIITPDQFLAPASTENILGVPLQGLTSSDRLRCFYSGDV 107
Db 83 TQADLHLLPLANETLILHMAHSYFLAPLVYVRRHRRDRTSPPLTRILNCHFGYK 142
Oy 108 NAEPSFRAVSLCGL-----RGATGYRAEYVISP L-----PNASA 144
Db 143 RGPATVNAISTCAGLSCNPFVLPRLITLCQVGHITRTAGNEYFIEBSKHEHPNGH 202
Oy 145 P-AAQRNS-OGAHLQNRG--VPGSPGD--PTSRGVSAGMNPALRALPYKPR-- 195
Db 203 PHVYFGSSVYKPKHSIKRNRKRKKGKSGSAGAEVSNCGTR-----EPRRM 248
Oy 196 -----AGFES 201
Db 249 ETRLEMOARGKVYQGGQRIIRNNNNNNNNNNKRYRHHQOIKSRVPTKKEVETQOTE 308
Oy 202 RSRRSRGRAKFVSLPRVETLVVADESVMYFNGADLENYLTLTLTAARLYRHPSTLNP 261

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Db 903 PLENNOSKAPBPLFMWHTSMEDCDATCGGGERKTTVSTCKTMSKNISIVDNCKKYLT 962
QY 830 ---NOVEQDDRR-PAARMVAGSWGSPASGSGSLQRAVDCRSAGORTYPAD-----AA 881
Db 963 KPEPQIRKCEQPCQTRMTEWTPTCSRTGCKMOSROVACTOOLNSGTLIRAREDCIG 1022
QY 882 HREVEFQAC-GEPCPT-WELSAWSPCSKSGCFORSLKCVGHGRLARDOCNLHRKP 939
Db 1023 PKHSAQRCGDCQCMTWEGVWSEFSVKCGKIRHRYACTN-----PRKCVLSTR 1076
QY 940 QELDFC 945
Db 1077 REAEDC 1082

RESULT 11
Q8WXS8 PRELIMINARY; PRT; 1223 AA.
AC Q8WXS8;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE A delta integrin-like and metalloprotease with thrombospondin type 1
DE motif 14 precursor.
GN ADAMTS14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21638061; Pubmed-11779638;
RA Bolz H., Ramirez A., von Bredlerow B., Kubisch C.;
RA "Characterization of ADAMTS14, a novel member of the ADAMTS
RT metalloprotease family";
RL Blochm. Biophys. Acta 1522:221-225(2001).
DR EMBL; AF358666; AAL40229.1;
DR Interpro: IPR002870; Rep_M12B_Proprep.
DR Interpro: IPR001590; Repolysin.
DR Interpro: IPR000884; TSP1.
DR Pfam: PF01562; Rep_M12B_Proprep; 1.
DR Pfam: PF01421; Repolysin; 1.
DR Pfam: PF00090; TSP_1; 4.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 1.
KW Signal; Integrin; Protease; Metalloprotease.
FT SIGNAL 1 22
FT SEQUENCE 1223 AA; 13871 MW; 36394ACAD92F170F CRC64;

Query Match 21.7%; Score 1122; DB 4; Length 1223;
Best local similarity 29.9%; Pred. No. 4.4e-84;
Matches 306; Conservative 122; Mismatches 379; Indels 216; Gaps 40;

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QY 331 GNADVGMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPD---NVKCEEVFKLRAN 387
Db 368 GYAPVGMCHPLRSCALNHEDGSSAFVIAHEGHVILGHMDGAGCADETSLG---- 423
QY 388 HNSPTLIQIDRANPWSACSAAITPDLDSGHDCLLDOPSKPI-SLPEDLPASVTL50 446
Db 424 -VVAFLVQAAPHFHMHSRCSKLELSRLPS- YDCLLDPEFDPAWPOPELPGLNYSME 480
QY 447 QCELAFGVSKPC---PYMOYCTKLMCTGAKAKOMVCOTNHPWADGTSCEBEKLLKGA 503
Db 481 QCRFDGSGYOTCLAFRTPEPCQWLCS-HPDNPYFCQTKKGPRLDTECAPKWFKGH 539
QY 504 CYERHMLINKRHVDGSMKMDPYPCSTGCGGYOLARRQCTNTPANGKCYGCVARKYR 563
Db 540 CIKSPQYITGDDGWSMPTKFGSCRSKCGGYRVSRSNNPSPAYGGRPLGPMREYQ 539
QY 564 SCNLEPCPSSASGSKSFREQCEAFNGY-----NHSTNRLTLAVAVPKYSGVSPDKCK 617
Db 600 VCNSECPGY--EDFRAQCAKRNXYVHQNAKHS-----WVP-YEPDDAQKCE 647
QY 618 LIRANGTGYFYLAARKVYDGLCS-PDSTSVCGGKCIAGCDGNLGSKKRPDKGCVG 676
Db 648 LICQADTGDVPEMNOVYHDGTCTSYRDPYVCARGCVGVGCDKEVSKKADKCGVCG 707
QY 677 GDNKSKKYTGLETK--PMHGYNFVAIPAGASSIDIRQRYGLTGDNYLALKNS-QG 733
Db 708 GDNHCRVAGTGLGKASKQAGALKVQIPAGAHIO-----EALSKSPRIYVKNQVYG 762
QY 734 KYLLN-GHFVSAVERDOLVYKSLRLYSGTGAVESLQASRPLEPLIVEVLSVGKMP 791
Db 763 SFILNRGK--EATSKTFAMG-LWEWADVEDAKESLTKSGPLPEALIAL----- 811
QY 792 PVRYSFYLRKEPREDKSSHXPDRGPS-----YHNSVLSL--SNQY--EOPDRRP 840
Db 812 -----PRTEGPRSSLAKEYIHEDLLPLIGSNVLEBMD---T 848
QY 841 ARWVAGSWGSPASGSGSLQRAVDCR----- 867
Db 849 YEMALSKMAPCSKACGGGIGFTKYGCRRRDHHNVQNLCDHKRKPRIRRRCNQHPSCQ 908
QY 868 -----GSAGRT-----VACDAHNPVETOAC-----EPC 894
Db 909 PWWTEEMGACSRSCGLGVOTRGIOCLLPLSNGTHNVPMAKACAGAPRARRPCLRVPC 968
QY 895 PT-WELSAWSPCSKSGCFORSLK-----VGHGRLARDOCNLHRKPOELDPCVL 947
Db 969 PAQHRIGAMSGCSATGEGIQOROVYCRTNANSLSH-----CGDR-PDVIQVCSL 1018
QY 948 RPC 950
Db 1019 PAC 1021

RESULT 12
Q8TEY8 PRELIMINARY; PRT; 1159 AA.
AC Q8TEY8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
GN ADAMTS14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21839041; Pubmed-11741898;
RA Colige A., Vandenberghe I., Thiry M., Lambert C.A., Van Beeumen J.,
RA Li S.W., Prockop D.J., Lapiere C.M., Nussgens B.V.;
RA "Cloning and Characterization of ADAMTS-14, a Novel ADAMTS Displaying

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DB 540 CWMKSPQRTYGDGGWSSWTKFCSCGCGVRSRSRSCNNPSPAYGGFPLGPMFEYQ 599
564 SCNLEPCSPSASAKSFREOCEAFNGY-----NHSTNLTLLAVANVPYSGVSPDKOK 617
600 VCNSECEPPTY--EDFRAQCCAKRNSYYVHQAOKS-----VVP--YEPDDAOKCE 647
618 LICRANGTGYFYVLAKRVNDGTLCS--PDSTSYCVQCKICAKCGDNIGSKKRPDKCGVCG 676
648 LIGQSDTDGVDYPMQNVHDGTRCSYRDYISVARECEYVPGCDKEVSKKADKCGVCG 707
677 GDNKCKKVTGFTK--PMHGYNFVAIPAGASSIDIRQRYKGLIGDDNYALKNS--QG 733
708 GDNHCRRTVGTGKASKAGALKLVQIPAGARIQI-----EALKSPHRIYVKKQVYG 762
734 KYLLN--GHFVVSAREDLVVKSLRISGTGAVESLSQARILEPLVEVLSVKMTP 791
763 SFLLNPKGK---EATSRFTTAMG--LEMEDAVEDAKESLKTSGPLPEALIAL-- 811
792 PRVRSFYLPKEPREDKSSHHPKDPGRPS-----VLHNSVLSL--SNQY--EQPDDRP 840
812 -----PRTEGPRSLAKYVYIHEDLPLISNNVLEMD---T 848
841 ARNVAGSWGPCSASGSGLOKRAVDCR----- 867
849 YEMALSMAPCSKACGSGIETKYGCRRRRDHMHVHRLCDHKRKPPIRRSNQHPCSQ 908
868 -----GSAGORT-----VPACDAHHPVETOAG-----EPC 894
909 PVMVTEBWKACSYGKLGVTGTRDCLPLSLNGTHVKMAKACAGDRPARRCLRVPC 968
948 RPC 950
969 PAMRIGAMSGCATGEGIGIQRYVCRTNANSLGH-----CEGDR--PTVQVCSL 1018
1019 PAC 1021

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RESULT 14

096L37 PRELIMINARY; PRT; 1427 AA.

AC 096L37; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Von Willebrand factor-cleaving protease precursor.

GN ADAMTS13.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

RN 11

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX PubMed=11557746;

RA Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E., Fujikawa K.;

RT Structure of von Willebrand factor-cleaving protease (ADAMTS13), a metalloprotease involved in thrombotic thrombocytopenic purpura.

RL J. Biol. Chem. 276:41059-41063(2001).

DR EMBL: AY055376; AAL17652.1; -

DR MEROPS: M12.241; -

DR InterPro: IPR001590; Reprolysin.

DR InterPro: IPR000884; TSP1.

DR InterPro: IPR00130; Zn_MTPeptide.

DR Pfam: PF01421; Reprolysin; 1.

DR Pfam: PF00090; tsp_1; 4.

DR PROSITE: PS00215; ADAM_MERPRO; 1.

DR PROSITE: PS00092; TSP1; 1.

DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.

KW Protease; Signal.

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FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE.
SQ SEQUENCE 1427 AA; 153632 MW; EB1BC3AABCI4442 CRC64;
Query Match 17.3%; Score 893.5; DB 4; Length 1427;
Best Local Similarity 29.2%; Pred. No. 5,7e-65;
Matches 250; Conservative 108; Mismatches 347; Indels 151; Gaps 34;

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174 CGVASG-WNP-----ALTRALDPY-----KPRRAGFGESSRRSRGAKRP 213

21 CGFLLCWGRSHFQOGLALEPQAVSVSLSPAPLKGRRPSFGQROQROR-----RA 75

214 VSIPIRVETLVVADESMVRFGADLEHYLLTLATARLYRHPSTLNPINIVYKVLNR 273

76 AGGILHLELLVAAGPVDVFOAHQEDTERVYLTNLNIGELLRDSLSLQAFVHLVKKVILT 135

274 DRDSGRKYVGNALTLRNFCAMOKKLTKVSDKRPYWDAILFTRODL--CGATTCPTLGM 332

136 EPEGAPNITANLSSLSLVCGWSQTIPEDDTPGHADLVLYTRDLELPDGNROVRY 195

333 ADVGTMCDDPKRSCVIEDDLPSAFTTAHELGHVFNPHDNVRYCEVEFGKLRANHMSP 392

196 TOLGACSPYWSCLITIEDTFCGLVITAHETIGHSFLEHNGARGS-----CGGSGHYMAS 251

393 TLIQIDRANP-----WSACSAALITDFLDSGHDCCLD---QSPKPTSLPEDLPGASYT 443

252 -----DGAAPRAGLAWSPCSRROLLSLISGARCVWDPRPQGSAGHPDPAQGLYXS 306

444 LSOQCELAGVSGKPCPY-----MOTCTKLCTKAKAGQWVCOIRHFPMDGTSGEGKLC 439

307 ANEQCRVAEGPKAVACTFAREHLDMCOALSHTPDQSSRLVPLDGTGCGVEKWC 366

500 LKGCAYERHNLNK--HRVDSMAKMDPYGPCSRTCGGVQOLARRQCTNPTPANGKCEGV 558

367 SKGRCSLYELTPITIAVHGMSSMGSRSPSCRCGGVYTRRQCNPRAPFGGRACVGA 426

559 RVKRYSCNLEPCPSASGKSFREOCEAFNG-----YNHSTNLTLLAVAN--V 604

427 DLQEMCNTOACBKTO--LEFMSQCARTDGQPLRSSPGGASFYH-----MGAAY 474

605 PKTSGVSPRDKCLICRANGTGYFYVLAKRVNDGTLCSL-----DST--SYCVQGKCIKAG 658

475 PHSQGA--LCRHMCRAIGESFTMKRGDSFLDGTROMPGPREDDGLSLCVSGSCRTFG 531

659 CDGNLGSKRREDDCGVCGDGNKCKKVTGLET--KPMHGYNFVAIPAGASSIDIRQRY 716

532 CDGRBMSQVWMDKCYOYCGDGNSTCSPKSGFTAGRAEYVTFPLVTP--NLTSYI--ANH 588

717 KGLIGDNYLALKNSQKYLNLNGHFVVS--AVERDLVVKSL--LRYSGTGAVESLSQASR 773

589 RPLF---THLAVRIG--GRYVAKKMSISPTWTYPSLLEDGRVEYRVALLTDRLPLEIEIR 644

774 ---PILEPLVEYL-----SVGKMTPRVRYSTYLPKEPREDKSSHHPKDPGRGFSVLHNSV 825

645 IMGPLQEDADIDIOVRRYGEYGNLTRDITFTFYQPK----- 681

826 LSLSNQVEQDDPPARWV--AGSMGPCSASGSGLOKRAVDCGSAGQRTVPA--CDAH 882

682 -----PROAMVAALVARGCSVSCGAGLRVAVNSCLDQAKELVETVYQCGSQ 728

883 R-EVETQACG-EPCPT--WELSAWSPCSKSGRFORSLKCVGHGRL-----ARDQCN 934

729 QPAPWPEACVLEPCQPYWAVAGDGFPCASGCGGLRERPVACVEAGSLTLTPPARCAG 788

935 LHKRPDELFCVLRPC 950

789 AQPAPVALLTCNPOPC 804

RESULT 15

09GL54 PRELIMINARY; PRT; 269 AA.

ID 09GL54

AC 09GL54;


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Db 241 YLTLTAAARLYRHPSTLNPNINIVVAVVLLLRDSDSPKVTGNALTLRNFCAMOKKLN 300
OY 301 KVSDEHPYMDTAILEFTRODLCGATTCDTLGMADVTCMDPRSCSVYEDDGLPSAFTTA 360
Db 301 KVSDEHPYMDTAILEFTRODLCGATTCDTLGMADVTCMDPRSCSVYEDDGLPSAFTTA 360
OY 361 HELGHVFNMPHDNVKVCSEVEFGKLRANHMSPDLLQIDRANPWSACSAIITDFLDSHG 420
Db 361 HELGHVFNMPHDNVKVCSEVEFGKLRANHMSPDLLQIDRANPWSACSAIITDFLDSHG 420
OY 421 DCLLDQPSKPISTLPEDLFGASTYLSQOCELAFGVSKPCPYMOYCTKLMCTGKAKGQWVC 480
Db 421 DCLLDQPSKPISTLPEDLFGASTYLSQOCELAFGVSKPCPYMOYCTKLMCTGKAKGQWVC 480
OY 481 QTRHPFMAADGTSCGEGKCLCLGACACVERHNLNKHRVDSGMAKMDPGRPCSRCCGGVQTLAR 540
Db 481 QTRHPFMAADGTSCGEGKCLCLGACACVERHNLNKHRVDSGMAKMDPGRPCSRCCGGVQTLAR 540
OY 541 RQCTNPFPANGKCYCEGVRYKRSCLNBPCCPSASGKSFREOCFAFNGYNHSTNRLTLA 600
Db 541 RQCTNPFPANGKCYCEGVRYKRSCLNBPCCPSASGKSFREOCFAFNGYNHSTNRLTLA 600
OY 601 VAWPKYIGVSPROCKCLICRANGTYTYVLA PKVVDGTLCSPDSTSVCOGKCIKACGD 660
Db 601 VAWPKYIGVSPROCKCLICRANGTYTYVLA PKVVDGTLCSPDSTSVCOGKCIKACGD 660
OY 661 GNLSKRRFDCGVCYGDNKSKCKVTGTFTRPMHGYNFVAIPAGASSIDIRORGYKGLI 720
Db 661 GNLSKRRFDCGVCYGDNKSKCKVTGTFTRPMHGYNFVAIPAGASSIDIRORGYKGLI 720
OY 721 GDDNTLAKNSQKYLNGHFVVSVERDLYVKGSLRYSGTGAVESLQASRPILLEPLT 780
Db 721 GDDNTLAKNSQKYLNGHFVVSVERDLYVKGSLRYSGTGAVESLQASRPILLEPLT 780
OY 781 VEVLVSGKMPBPVRYSTYLPKEPREDEKSHPKDRGSPVLAHNSVLSNOVEDDDDBPP 840
Db 781 VEVLVSGKMPBPVRYSTYLPKEPREDEKSHPKDRGSPVLAHNSVLSNOVEDDDDBPP 840
OY 841 ARWAVSGWPCASGSGSLQKRAVDCRGSAGQRTVPACDAHNPETQACGEPCTTWLS 900
Db 841 ARWAVSGWPCASGSGSLQKRAVDCRGSAGQRTVPACDAHNPETQACGEPCTTWLS 900
OY 901 AWSPCSKSCGFGFQRRSLKCYHGGRLLARDQCNLHRRKPEQLDPCVLRPC 950
Db 901 AWSPCSKSCGFGFQRRSLKCYHGGRLLARDQCNLHRRKPEQLDPCVLRPC 950

```

RESULT 2

```

US-10-163-316-2
: Sequence 2, Application US/10163316
: Publication No. US20020197703A1
: GENERAL INFORMATION:
: APPLICANT: Kapellier-Libermann, Rosana
: TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase and Uses
: TITLE OF INVENTION: Therefor
: FILE REFERENCE: MPI01-025PIRNM
: CURRENT APPLICATION NUMBER: US/10/163,316
: CURRENT FILING DATE: 2002-06-05
: PRIOR APPLICATION NUMBER: 60/297,863
: PRIOR FILING DATE: 2001-06-13
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 823
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-163-316-2

```

```

Query Match 82.2%; Score 4242.5; DB 9; Length 823;
Best Local Similarity 96.9%; Pred. No. 5.5e-295;
Matches 791; Conservative 0; Mismatches 2; Indels 23; Gaps 1;

```

```

OY 1 MLLGILTLAPAGTAGGEFEEREYVPIRLDPDINGRRYYWRGEDSGDGLIQTATF 60
Db 1 MLLGILTLAPAGTAGGEFEEREYVPIRLDPDINGRRYYWRGEDSGDGLIQTATF 60
OY 61 QEDFLHLTPDAQFLAPAFSTEHGLVPLQGLTGSSDLRCFYSQDVAAEDSPAASLCL 120
Db 61 QEDFLHLTPDAQFLAPAFSTEHGLVPLQGLTGSSDLRCFYSQDVAAEDSPAASLCL 120
OY 121 GGLRGAFYRGAEYVISP LPNAPAPAO RNSOGAHLORRGVPGGSPDPTSRGVASGW 180
Db 121 GGLRGAFYRGAEYVISP LPNAPAPAO RNSOGAHLORRGVPGGSPDPTSRGVASGW 180
OY 181 NPAILRALDPYKPRRAGGSESRRRSGRARFVSIPTVETLVVADESNVYKFRGADLEH 240
Db 181 NPAILRALDPYKPRRAGGSESRRRSGRARFVSIPTVETLVVADESNVYKFRGADLEH 240
OY 241 YLTLTAAARLYRHPSTLNPNINIVVAVVLLLRDSDSPKVTGNALTLRNFCAMOKKLN 300
Db 241 YLTLTAAARLYRHPSTLNPNINIVVAVVLLLRDSDSPKVTGNALTLRNFCAMOKKLN 300
OY 301 KVSDEHPYMDTAILEFTRODLCGATTCDTLGMADVTCMDPRSCSVYEDDGLPSAFTTA 360
Db 301 KVSDEHPYMDTAILEFTRODLCGATTCDTLGMADVTCMDPRSCSVYEDDGLPSAFTTA 360
OY 361 HELGHVFNMPHDNVKVCSEVEFGKLRANHMSPDLLQIDRANPWSACSAIITDFLDSHG 420
Db 361 HELGHVFNMPHDNVKVCSEVEFGKLRANHMSPDLLQIDRANPWSACSAIITDFLDSHG 420
OY 421 DCLLDQPSKPISTLPEDLFGASTYLSQOCELAFGVSKPCPYMOYCTKLMCTGKAKGQWVC 480
Db 421 DCLLDQPSKPISTLPEDLFGASTYLSQOCELAFGVSKPCPYMOYCTKLMCTGKAKGQWVC 480
OY 481 QTRHPFMAADGTSCGEGKCLCLGACACVERHNLNKHR-----VDG 517
Db 481 QTRHPFMAADGTSCGEGKCLCLGACACVERHNLNKHRPTDIISPKDLLRLPGLHTTQYDG 540
OY 518 SMAKMDPYGPCSRCCGGVQTLARROCTNPFPANGKCYCEGVRYKRSCLNBPCCPSASGK 577
Db 518 SMAKMDPYGPCSRCCGGVQTLARROCTNPFPANGKCYCEGVRYKRSCLNBPCCPSASGK 577
OY 578 SFREOCFAFNGYNHSTNRLTLA VAWPKYIGVSPROCKCLICRANGTYTYVLA PKVVD 637
Db 578 SFREOCFAFNGYNHSTNRLTLA VAWPKYIGVSPROCKCLICRANGTYTYVLA PKVVD 637
OY 601 SFREOCFAFNGYNHSTNRLTLA VAWPKYIGVSPROCKCLICRANGTYTYVLA PKVVD 660
Db 601 SFREOCFAFNGYNHSTNRLTLA VAWPKYIGVSPROCKCLICRANGTYTYVLA PKVVD 660
OY 638 GTLCSPDSTSVCOGKCIKACGDNLSGKRRFDCGVCYGDNKSKCKVTGTFTRPMHGYN 697
Db 638 GTLCSPDSTSVCOGKCIKACGDNLSGKRRFDCGVCYGDNKSKCKVTGTFTRPMHGYN 697
OY 661 GTLCSPDSTSVCOGKCIKACGDNLSGKRRFDCGVCYGDNKSKCKVTGTFTRPMHGYN 720
Db 661 GTLCSPDSTSVCOGKCIKACGDNLSGKRRFDCGVCYGDNKSKCKVTGTFTRPMHGYN 720
OY 698 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVVSVERDLYVKGSL 757
Db 698 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVVSVERDLYVKGSL 757
OY 721 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVVSVERDLYVKGSL 780
Db 721 FVVAIPAGASSIDIRORGYKGLIGDDNTLAKNSQKYLNGHFVVSVERDLYVKGSL 780
OY 758 RYSGTGAVESLQASRPILLEPLTVEVLVSGKMPBP 793
Db 758 RYSGTGAVESLQASRPILLEPLTVEVLVSGKMPBP 816

```

RESULT 3

```

US-09-321-987B-4
: Sequence 4, Application US/09321987B
: Patent No. US20020102210A1
: GENERAL INFORMATION:
: APPLICANT: Kinble, Judith E
: APPLICANT: Bielloch, Robert H
: TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
: FILE REFERENCE: 960296.93386
: CURRENT APPLICATION NUMBER: US/09/321,987B
: CURRENT FILING DATE: 1999-05-28
: PRIOR APPLICATION NUMBER: 60/087,170
: PRIOR FILING DATE: 1998-05-29
: PRIOR APPLICATION NUMBER: 60/129,023
: PRIOR FILING DATE: 1999-04-13
: NUMBER OF SEQ ID NOS: 5

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Db 640 ECRDINGO---PASECAKEVPASTRPCADHPQWOLGEMSSCSKTCGKGRKRSIKCL 696

QY 922 GHGGRLARDOCNLHRRKPOE-LDFCVLRPC 950

Db 697 SHDGGVLSHESCPLKKPKHIFDICTLTQC 726

RESULT 8

US-09-445-023A-1

; Sequence 1, Application US/09445023A

; Patent No. US20020119167A1

; GENERAL INFORMATION:

; APPLICANT: Hirose, Kunitaka

; APPLICANT: Inoguchi, Ei-ji

; APPLICANT: Hakozaaki, Michinori

; APPLICANT: Ishioaka, Keiko

; APPLICANT: Matsushima, Yukako

; APPLICANT: Kuno, Kouji

; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

; FILE REFERENCE: 057092

; CURRENT APPLICATION NUMBER: US/09/445,023A

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: JP 9-160422

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 727

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-445-023A-1

Query Match 44.0%; Score 2274; DB 10; Length 727;

Best Local Similarity 54.4%; Pred. No. 2, 2e-154;

Matches 408; Conservative 129; Mismatches 173; Indels 40; Gaps 11;

QY 209 RAKREVSIRPYVETLVVADESWMKFRGADLEHLLTLTAARLYRHSILNPINIVYVK 268

Db 9 RKRREVSIRPYVETLVVADESWMKFRGADLEHLLTLTAARLYRHSILNPINIVYVK 68

QY 269 VILLRDRDQSGPKYTGNAALTLRNFCAWOKLNVSDKHREYMDTALFTRODLCGATCD 328

Db 69 ILVTHDQKREYTSNAALTLRNFCAWOKLNVSDKHREYMDTALFTRODLCGATCD 128

QY 329 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPDNYKCEVEFGKLRANH 388

Db 129 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPDNYKCEVEFGKLRANH 188

QY 389 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDPSKPLSLPDLPGASVYTLISQOC 448

Db 189 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDPSKPLSLPDLPGASVYTLISQOC 248

QY 449 ELAFVGSRPCP-YMOCYTKLWCTGKAKGQWVOTRHPFADTSGEGKLCIKGACVER 507

Db 249 QTFEGEDSHCPDASTCTTLWCTGSGVLVCQTKHFPWADTSGEGKLCIKGACVER 308

QY 508 HNLNKH---RVDSMAKMDPYGPCSRCTGGVQLARRCCTNPTPANGKRYCEGVYKYS 564

Db 309 TD-RKHFDPFRHSGMGPWGMGDCSRTCGGVOYTRMRECDNPYPKAGGKCYCEKRYKYS 367

QY 565 CNLEPCPSASGKSPREDOCEAFNGYHSTNRLTLAVAWPKYSGVSPRDKCLICRANG 624

Db 368 CNLEPCPSASGKSPREDOCEAFNGYHSTNRLTLAVAWPKYSGVSPRDKCLICRANG 426

QY 625 TGFVYLAKRYVDGTICSDPSTSVYCQKICRACGCGNIGSKRPRKCYGCGDNKSCCK 684

Db 427 IGTFEVLQKRYVDGTICSDPSTSVYCQKICRACGCGNIGSKRPRKCYGCGDNKSCCK 486

QY 685 VTGLFTKPMHGYVFAIPAGASSIDIRGKYGILGIDNNTALAKNSQKYLINGFVYS 744

Db 487 ISSSVTSAPRGHDIYITITGATINIEVKORNGSRNNSFLAKADGTYIINGDYTIS 546

QY 745 AVERDLVKGSLIRYSGTAVESLOASRPLTEPLVEVLYSGKMPPRYRFTYLPKEP 804

Db 547 TLEODIMTKGVLYRYSGLALERKNSFPLKEPLTQVLTGALRPLKTYTFYVARK- 605

QY 805 REDKSSHPKDRGSPVJHNSVLSLNOVEQPDPRPARWAGSWGPCSASGSLORAV 864

Db 606 ---KES-----FNLIPTFS-----AWIEMGECSSKSCGELGMORRLV 639

QY 865 DCRSGAQRTVPACDAH--RPVETQACGE-PCPTWLSMWSRCSKCGGFORRSIKCY 921

Db 640 ECRDINGO---PASECAKEVPASTRPCADHPQWOLGEMSSCSKTCGKGRKRSIKCL 696

QY 922 GHGGRLARDOCNLHRRKPOE-LDFCVLRPC 950

Db 697 SHDGGVLSHESCPLKKPKHIFDICTLTQC 726

RESULT 9

US-10-097-597-12

; Sequence 12, Application US/10097597

; Publication No. US20030022352A1

; GENERAL INFORMATION:

; APPLICANT: Hirose, Kunitaka

; APPLICANT: Inoguchi, Ei-ji

; APPLICANT: Hakozaaki, Michinori

; APPLICANT: Ishioaka, Keiko

; APPLICANT: Matsushima, Yukako

; APPLICANT: Kuno, Kouji

; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same,

; FILE REFERENCE: 057092

; CURRENT APPLICATION NUMBER: US/10/097,597

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: 09/445,023

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: JP 9-160422

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12

; LENGTH: 727

; TYPE: PRT

; ORGANISM: Mus sp.

US-10-097-597-12

Query Match 44.0%; Score 2273; DB 9; Length 727;

Best Local Similarity 53.7%; Pred. No. 2, 6e-154;

Matches 403; Conservative 131; Mismatches 176; Indels 40; Gaps 10;

QY 209 RAKREVSIRPYVETLVVADESWMKFRGADLEHLLTLTAARLYRHSILNPINIVYVK 268

Db 9 RKRREVSIRPYVETLVVADESWMKFRGADLEHLLTLTAARLYRHSILNPINIVYVK 68

QY 269 VILLRDRDQSGPKYTGNAALTLRNFCAWOKLNVSDKHREYMDTALFTRODLCGATCD 328

Db 69 ILVTHDQKREYTSNAALTLRNFCAWOKLNVSDKHREYMDTALFTRODLCGATCD 128

QY 329 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPDNYKCEVEFGKLRANH 388

Db 129 TLGMADVGTWCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPDNYKCEVEFGKLRANH 188

QY 389 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDPSKPLSLPDLPGASVYTLISQOC 448

Db 189 MMSPTLIQIDRANPWSACSAIITDPLDSGHGDCLLDPSKPLSLPDLPGASVYTLISQOC 248

QY 449 ELAFVGSRPCP-YMOCYTKLWCTGKAKGQWVOTRHPFADTSGEGKLCIKGACVER 507

Db 249 QTFEGEDSHCPDASTCTTLWCTGSGVLVCQTKHFPWADTSGEGKLCIKGACVER 308

QY 508 HNLNKH---RVDSMAKMDPYGPCSRCTGGVQLARRCCTNPTPANGKRYCEGVYKYS 564

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Db 309 TDM-KHFATPVHSGMGPWGMGDCSRTCGGVOYTMRECDNPVKNKGKCEGKRVYRS 367
Oy 565 CNIPEPCSSAGKSFREOCEAFNGNHNRLTLAVAWPKYSGVSPRCKLICRANG 624
Db 368 CNIEDCPDN-NGKTFREOCEAHNEFSKASFGNEPTVEMTPKYAGVSPKDRCLTCEAKG 426
Oy 625 TGFVYLPAPKVVYDGTLCSPDSTSVCGOKICKAGCDGNLSKKRFPDGCYCGGDNCKK 684
Db 427 IGFVYLPAPKVVYDGTLCSPDSTSVCGOKICKAGCDRIIDSKKFKDGCYCGGDNCKK 486
Oy 685 VTGLFTKPMHGYNFVAIPAASSIDIRORGYKGLIGDDNYLALKNQGYLLNGHVV 744
Db 487 MSGIVSTRPGYHDIYIPAGATNIEVKHNGSRNNGSFLAIRADGTIILNGNTLS 546
Oy 745 AVERDLVYKSLRSTGTGAVESLQASRILEPLVEVLSVGKMPRRYRISYLPKEP 804
Db 547 TLEODLTKYKTVLRYSSSSALERIRSFPLKEPLTQVLMVGHALRPKIKFYEMKKT 606
Oy 805 REDKSSHPKDRGPRSVLHNSVLSLNOVEQDDRRPARVAGSMGPCSAGSGLOKRAV 864
Db 607 ES-----FNALPTFS-----EWIIEEGESKTCGSGMORRV 639
Oy 865 DCRGSAGQRTVPACDAAH--RPVETOACGE-PCPTWELSAMSPSCSGRGFORSLKCV 921
Db 640 QCRDINGH---PASECAKEVKPASTRPCADLPCPHMQVGDMSPCSKTGKGYKRTLKV 696
Oy 922 GHGRLARQCNLHRRPOE-LDPCVLRPC 950
Db 697 SHDGVLSNESCDPLKKPKHYIDFCTLQOC 726
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RESULT 10
US-10-097-580-12
; Sequence 12, Application US/10097580
; Publication No. US20030032168A1
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Ei-ji
; APPLICANT: Hakozaeki, Michinori
; APPLICANT: Ishioke, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: 057092
; CURRENT APPLICATION NUMBER: US/10/097,580
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 09/445,023
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-097-580-12
```

```
Query Match 44.0%; Score 2273; DB 9; Length 727;
Best Local Similarity 53.7%; Pred. No. 2,6e-154;
Matches 403; Conservative 131; Mismatches 176; Indels 40; Gaps 10;
Oy 209 RAKRFVSIPIRYVELLVVADSMKFRGADLEHYLLTLATRAARXRRPSILNPINIVYK 268
Db 9 RKRFRVSSPIRYVELTMAVDOSMAFHSGLKHYLLTLEFVAARYYKHPSTIRNSISLVYK 68
Oy 269 VLLLRDSDGPKVYGNALTLRNCAQKLNKYSDKHPEYWDPAIIFTRDOLCGATCCD 328
Db 69 ILVYEBQKGPVYSNALLRLRNCSWQKOHNSPDRDPEHYDAIILFTRODLGCSHTCD 128
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Oy 329 TLGMADVTCMDPKRSCSYLEDGLPSAFTTAHELGHVFNMPHNDNVKCEBEVGLRANH 368
Db 129 TLGMADVTCMDPKRSCSYLEDGLPSAFTTAHELGHVFNMPHNDNVKCEBEVGLRANH 368
Oy 389 MMSPTLIQIDRANPMWASCAIITDPLDSGHGCLLDQSPKPSLPEBDLPGASYTSSQOC 448
Db 189 LMASMLSSLDHSPWSPSCSYVWYTSFLDNGHGLMDKPNPNTKLPSPDLTGLTYDANROC 248
Oy 449 ELAFVGSKPCP-YMGYCTFLMCTGKAKGOMQOTRHPADDTSCGEGKTLCKGACVER 507
Db 249 QFTFGESEKHPDAASTCTILMCTGTSGLLVCOIKHFPADDTSCGEGKTCVSGKCVNK 308
Oy 508 HNINKH---RVDSMAKMDPYGPCSRTCGGVOYLARROCTNPTPANNGKRYCEGVRYRS 564
Db 309 TDM-KHFATPVHSGMGPWGMGDCSRTCGGVOYTMRECDNPVKNKGKCEGKRVYRS 367
Oy 565 CNIPEPCSSAGKSFREOCEAFNGNHNRLTLAVAWPKYSGVSPRCKLICRANG 624
Db 368 CNIEDCPDN-NGKTFREOCEAHNEFSKASFGNEPTVEMTPKYAGVSPKDRCLTCEAKG 426
Oy 625 TGFVYLPAPKVVYDGTLCSPDSTSVCGOKICKAGCDGNLSKKRFPDGCYCGGDNCKK 684
Db 427 IGFVYLPAPKVVYDGTLCSPDSTSVCGOKICKAGCDRIIDSKKFKDGCYCGGDNCKK 486
Oy 487 MSGIVSTRPGYHDIYIPAGATNIEVKHNGSRNNGSFLAIRADGTIILNGNTLS 546
Oy 745 AVERDLVYKSLRSTGTGAVESLQASRILEPLVEVLSVGKMPRRYRISYLPKEP 804
Db 547 TLEODLTKYKTVLRYSSSSALERIRSFPLKEPLTQVLMVGHALRPKIKFYEMKKT 606
Oy 805 REDKSSHPKDRGPRSVLHNSVLSLNOVEQDDRRPARVAGSMGPCSAGSGLOKRAV 864
Db 607 ES-----FNALPTFS-----EWIIEEGESKTCGSGMORRV 639
Oy 865 DCRGSAGQRTVPACDAAH--RPVETOACGE-PCPTWELSAMSPSCSGRGFORSLKCV 921
Db 640 QCRDINGH---PASECAKEVKPASTRPCADLPCPHMQVGDMSPCSKTGKGYKRTLKV 696
Oy 922 GHGRLARQCNLHRRPOE-LDPCVLRPC 950
Db 697 SHDGVLSNESCDPLKKPKHYIDFCTLQOC 726
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RESULT 11
US-09-445-023A-12
; Sequence 12, Application US/09445023A
; Patent No. US20020119167A1
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Ei-ji
; APPLICANT: Hakozaeki, Michinori
; APPLICANT: Ishioke, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: 057092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-445-023A-12
```

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Query Match 44.0%; Score 2273; DB 10; Length 727;
```


RESULT 13
 US-09-972-467-2
 ; Sequence 2, Application US/09972467
 ; Patent No. US20020090373A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PEIER INC.
 ; TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: PCI0850A
 ; CURRENT APPLICATION NUMBER: US/09/972,467
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 1629
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-972-467-2

Query Match 38.1%; Score 1965; DB 10; Length 1629;
 Best Local Similarity 39.9%; Pred. No. 7.7e-132;
 Matches 411; Conservative 145; Mismatches 351; Indels 122; Gaps 21;

QY 22 EREVVPRLDP-----DINGRRYV-----RGPEDSGQGLIFQITAFQ 61
 DB 47 EYEIPIRVNMLGEPPTNVHFKTRRSINATDPMFAFASSSSSTSOAHYRLSAG 106
 QY 62 EDVYHLTPDAQFLAPAESTEHLGVP---LQGLTGSSDLRCFCYSGDVNAEPDSFAAV 117
 DB 107 QOFLFLTNAGFIAPLFTVLTGTPGVNQTKFYSEEAELKHCFKGYGVNTNSEHTAVI 166
 QY 118 SLCCGLRGAFYRGAEYISPLPMASAPAAQNSGAILHLLQRYGVGGSGDPTSCGVA 177
 DB 167 SLCSGMLTFRSHDGYFTPLQSMDEQDEEQNKPHIYRSAPQREPTSGRAHCDTS 226
 QY 178 SCMNPAILLALDPYKPRAGFGE-----SRSRRSG 208
 DB 227 EHKN---RHSKKKTRAKMGERINLADVAALNSGLATEAFSAVGNKTDNTRERTRR 283
 QY 209 RAKREYSIRYVELTVADENSVKREHGADELHYLLTLTAARLYNHSILNPINIVYK 268
 DB 284 RKRRELSYRFEVLLVADNRVSYGENILOHLYITLMSIVASYDPSIGNLINIVIVN 343
 QY 269 VLLLRDSDPYVTGNAALTLNFCAMOKLKNVSDKHPEYMDTALFTFRODLGCA-TTC 327
 DB 344 LIVIHNEQDGPSTISFAOITLKNFCOMQHSKSPGSIH---HDTAVLLTRDICTRAHDKC 400
 QY 328 DTLGMADVGTMCDPKRSQVIEDDGLPSAFTTAHELGHVFNMPHDNVKCEEVFGKLRAN 387
 DB 401 DTLGLAELGTICDPYKSCISEDSGLSTAFTIAHELGHVFNMPHDNNKKEE-GVKSPO 459
 QY 388 HMASPLIIDIRANPMWASCSAAITDFLDSGHDCILDP-SKPISLPEDLDGASTLSQ 446
 DB 460 HMAAPLNLNYPNMMWMSKSRKYTEFLDTGCECLNBPESRPYLPOLPILILNVNK 519
 QY 447 OCELAGVSGKPCPYMOYCTKLKMC---TGKAGOMVCOYTRHPMADTSCGSEKLLDKA 503
 DB 520 OCELITGSPSYOCYPMOCRLKCNVNVHKG---CRQHTPMAGTCEPEKHKHXYG 576
 QY 504 CVERHNLNHRVYDGMWAKWDPYGCPSRTCGGCVOLARROCTNPTPANGSKYCEGVVYK 563
 DB 577 CVPK-EMDVPVTDGWSGSSPFGTCSRTCGGKIKTAIRCNRPKNGKGYCVGRMKR 635
 QY 564 SCLEPCPSASGKSFREGQCEAFNXYNSTNLTLAVAMVPKYSVSVSRDCKKLICRAN 623
 DB 636 SCETPECLKOK--RDFRDOCAHFDEKHNINGLRNVHVPYSSILMKDRKLCRYA 693
 QY 624 GYGYFVLPARKVVDGLCPDSTSVYCGKICAKGCDNLGSKRKDKCYCGGDKSK 683
 DB 694 GNTAYQLADRVLDGTTPCCODTNDICVGLCRAGCDHNLNARDKCYCGGDSCK 753
 QY 684 KYTGLETFKPMHGYNVVAIPAGASSIDIRQGYKGLIGDNTYALAKNSQKYLNGHFV 743

DB 754 TVAGTFNVHYGYNTVRLPRAGATINDVRQHSFSETDDNDLALSSSGEFLNGNFV 813
 QY 744 SAVERDLVYKGLLRYSGTGAVESLQASRPILLEPLTYEVLSVGMTPRVRYSFLPKE 803
 DB 814 TMAKREIRIGNAVYSESGEFAVERINSTRIEQELLQVLVSVKLYNDPVRYSPNIPLE 873
 QY 804 PREDK---SHPKDRGP-----SVLHNSVLSLNOVEQDDPP-- 840
 DB 874 DKPQGFYWNHSH---GPMQACSKPCQGERKKRLVCTRESQDLYVS---DQRCRLPQPG 925
 QY 841 -----ARWVAGSWGPCSASCGLQKRAVDCR-----GSAGRTVPACDAHR 883
 DB 926 HTEPCGTDCLDRHNVHVASSECSAOCGLYRLDITICAYSRLDKTEKVDGFCSSHPK 985
 QY 884 PVETQACGEPT--WEISAMSPCSKSGRFGORSCLKVGHGRLARDQNLHRKPOE 941
 DB 986 PSNRKCSGECNTGMWRYSAMTECSKCDGTYORRALCYNTRNDVLDOSKCT-HQEKVT 1044
 QY 942 LDFCYLAPC 950
 DB 1045 IQRCSEFPC 1053

RESULT 14
 US-10-174-590-352
 ; Sequence 352, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior application removed - See file wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 352
 ; LENGTH: 837
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-174-590-352

Query Match 37.1%; Score 1916; DB 9; Length 837;
 Best Local Similarity 46.3%; Pred. No. 1e-128;
 Matches 381; Conservative 123; Mismatches 267; Indels 52; Gaps 16;

QY 1 MLILGLTLAFAGRTAGFEPREVVVPIRLDPDINGRRYVMPGDSGQGLIFQITAF 60
 DB 37 LILLILASLLPSARLASPLPREELVFPKLSVY-----PSGAPARILCRLOAF 88
 QY 61 OEDFVYHLTPDAQFLAPAESTEHLGVP-LQGLTGSSDLRCFCYSGDVNAEPDSFAAVSLIC 120
 DB 89 GETLLELDQDSGVYEGVLTGYLQGAPE-LLGAPAP--GYTLGTITNGDPESVASLHMD 145
 QY 121 GG-LRGAFGYKGAEYIYISPLPMASAPAAQNSGAILHLLQRYGVGGSGDPTSRGCVASG 179
 DB 146 GGALGVLQYRGAEHLQPLEGTPNSA--GGPGAILRRK---SPASQGFMCNV--- 196
 QY 180 MNPAILLALDPYKPRAGGESRRSGRAKRFVSIIPRVETLVVADENSVKREHGADEL 239
 DB 197 -----KAPIGSPSPRPR--RAKRFASLSRFVETLVVADDMAAFHQAIGLK 239

